SEQUENCE LISTING

<111> Brennan, Thomas J.

<120> TRANSGENIC MICE CONTAINING 5-HT-2B GENE
DISRUPTIONS

<130> R-599

<140> US 09/903,376
<141> 2001-07-10

<150> US 60/218,358
<151> 2000-07-12

<150> US 60/223,120
<151> 2000-08-07

<150> US 60/223,122
<151> 2000-08-07

<160> 4

<170> FastSEQ for Windows Version 4.0

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<213> Mus musculus

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ccctggaccg ctatatagcc atcaaaaagc caattcaggc caatcagtgc aacacccggg 540
ctactgcatt catcaagatt acagtggtat ggttaatttc aataggcatc gccatcccag 600
tccctattaa aggaatcgag actgatgtga ttaatccaca caatgtcacc tgtgagctga 660
caaaggaccg ctttggcagt tttatggtct ttgggtcact ggctgctttc ttcgtacctc 720
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catttggcag gtacatcacc tgcaattacc gagccacaaa gtcagtaaaa gcacttagga 1260
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gttcaaccat tcagtcctca tcaatcatcc tcctcgatac ccttctcact gaaaacgatg 1440
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<212> PRT
<213> Mus musculus

<400> 2

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Leu Glu Thr Asp Ser Val Ala Glu Glu Met Lys Gln Thr Val Glu Gly
            35                  40                  45
Gln Gly His Thr Val His Trp Ala Ala Leu Leu Ile Leu Ala Val Ile
        50                  55                  60
Ile Pro Thr Ile Gly Gly Asn Ile Leu Val Ile Leu Ala Val Ala Leu
65                  70                  75                  80
Glu Lys Arg Leu Gln Tyr Ala Thr Asn Tyr Phe Leu Met Ser Leu Ala
                85                  90                  95
Ile Ala Asp Leu Leu Val Gly Leu Phe Val Met Pro Ile Ala Leu Leu
            100                 105                 110
Thr Ile Met Phe Glu Ala Ile Trp Pro Leu Pro Leu Ala Leu Cys Pro
        115                 120                 125
Ala Trp Leu Phe Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met His
        130                 135                 140
Leu Cys Ala Ile Ser Leu Asp Arg Tyr Ile Ala Ile Lys Lys Pro Ile
145                 150                 155                 160
Gln Ala Asn Gln Cys Asn Thr Arg Ala Thr Ala Phe Ile Lys Ile Thr
                165                 170                 175
Val Val Trp Leu Ile Ser Ile Gly Ile Ala Ile Pro Val Pro Ile Lys
                180                 185                 190
Gly Ile Glu Thr Asp Val Ile Asn Pro His Asn Val Thr Cys Glu Leu
            195                 200                 205
Thr Lys Asp Arg Phe Gly Ser Phe Met Val Phe Gly Ser Leu Ala Ala
        210                 215                 220
Phe Phe Val Pro Leu Thr Ile Met Val Val Thr Tyr Phe Leu Thr Ile
225                 230                 235                 240
His Thr Leu Gln Lys Lys Ala Tyr Leu Val Lys Asn Lys Pro Pro Gln
                245                 250                 255
Arg Leu Thr Arg Trp Thr Val Pro Thr Val Phe Leu Arg Glu Asp Ser
                260                 265                 270
Ser Phe Ser Ser Pro Glu Lys Val Ala Met Leu Asp Gly Ser His Arg
            275                 280                 285
Asp Lys Ile Leu Pro Asn Ser Ser Asp Glu Thr Leu Met Arg Arg Met
        290                 295                 300
Ser Ser Val Gly Lys Arg Ser Ala Gln Thr Ile Ser Asn Glu Gln Arg
305                 310                 315                 320
Ala Ser Lys Ala Leu Gly Val Val Phe Phe Leu Phe Leu Leu Met Trp
                325                 330                 335
Cys Pro Phe Phe Ile Thr Asn Leu Thr Leu Ala Leu Cys Asp Ser Cys
                340                 345                 350
Asn Gln Thr Thr Leu Lys Thr Leu Leu Glu Ile Phe Val Trp Ile Gly
            355                 360                 365
Tyr Val Ser Ser Gly Val Asn Pro Leu Ile Tyr Thr Leu Phe Asn Lys
            370                 375                 380
Thr Phe Arg Glu Ala Phe Gly Arg Tyr Ile Thr Cys Asn Tyr Arg Ala
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385                 390             Phe Ser Ser Thr Leu Cys Phe
Thr Lys Ser Val Lys Ala Leu Arg Lys     410             415
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Gly Asn Ser Met Val Glu Asn Ser Lys     425             430
                420                 Tyr Gln Ser Pro Met Arg Leu Arg
Arg Asn Gly Ile Asn Pro Ala Met         445
                435                 440
Cys Ser Thr Ile Gln Ser Ser Ser Ile Ile Leu Leu Asp Thr Leu Leu
    450                 455                 460
Thr Glu Asn Asp Gly Asp Lys Ala Glu Glu Gln Val Ser Tyr Ile Leu
465                 470                 475             480
Gln Glu Arg Ala Gly Leu Ile Leu Arg Glu Gly Asp Glu Gln Asp Ala
                485                 490             495
Arg Ala Pro Trp Gln Val Gln Glu
                500
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<210> 3
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting vector

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taaaatgtct gaacaaagca caacttctga gcacatttta cagaagacat gtgatcacct 180
gatcctgact aaccgttctg                                            200


<210> 4
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting vector

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gtttggtgag tatttcccct tgttcctgcc actgaacact actaacgtag tgaaatggac 120
actcactgac ctttattttg tttgaaataa aagaaggacc tggattaaaa acacagaagg 180
gaacattcct tcatttttca                                            200
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